

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 25, 2002, 01:10:42 ; Search time 44 Seconds

(without alignments)
904.538 Million cell updates/sec

Title: US-09-708-724A

Perfect score: 2187

Sequence: 1 MGPSVVVLCMKQLGAL.....LLAVTREGLERRIISRRAE 414

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Missing first 45 summaries

Database :

PIR_73:
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	6.3	1460	1	EDBEIF
2	128	5.9	2517	2	S58380
3	121.5	5.9	1396	2	A44453
4	120	5.8	1386	2	T49316
5	117.5	5.4	1402	2	T46707
6	116	5.3	606	2	T51880
7	116	5.3	3149	1	Q0BE8
8	115.5	5.3	1335	2	T18289
9	114.5	5.2	501	2	S76563
10	114	5.2	1611	2	T38236
11	112.5	5.1	801	2	T29018
12	112	5.1	594	2	S33561
13	111	5.1	583	2	S29961
14	111	5.1	728	2	S43768
15	110.5	5.1	743	2	C56695
16	110.5	5.1	1012	2	I53172
17	110.5	5.1	1290	2	T00018
18	110	5.0	817	2	S51342
19	110	5.0	2142	2	B35098
20	109.5	5.0	590	2	S29964
21	109.5	5.0	1192	2	T18611
22	109	5.0	883	2	S49126
23	109	5.0	1246	2	G89287
24	108.5	5.0	771	2	T38616
25	108.5	5.0	938	2	T39006
26	108.5	5.0	1801	2	T26774
27	108	4.9	524	2	A75588
28	108	4.9	528	2	I47141
29	108	4.9	2187	2	T30826

30 107.5 4.9 1208 2 T27822
31 107 4.9 1188 2 JC4889
32 107 4.9 1260 2 S60896
33 107 4.9 1388 2 A53317
34 106.5 4.9 365 1 SAVLWE
35 106.5 4.9 834 2 T42702
36 106.5 4.9 1074 2 T24877
37 106.5 4.9 1076 2 T24887
38 106.5 4.9 3262 2 AH2137
39 106.5 4.9 5262 2 T03454
40 106 4.8 620 2 S06733
41 106 4.8 633 2 S62057
42 106 4.8 805 2 T49385
43 106 4.8 2361 2 T25752
44 105.5 4.8 626 1 NBHUIA
45 105.5 4.8 1210 2 T39410

ALIGNMENTS

RESULT 1

EDBEIF

Immediate-early protein IE180 - suid herpesvirus 1 (strain Indiana-Funkhauser)

C:Species: suid herpesvirus 1

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Feb-1997

C:Accession: S04713

R:Cheung, A.K.

Nucleic Acids Res. 17, 4637-4646, 1989

A:Title: DNA nucleotide sequence analysis of the immediate-early gene of pseudorabies

A:Reference number: S04713; MUID:89315207; PMID:2546124

A:Accession: S04713

A:Molecule type: DNA

A:Residues: 1-1460 <CHE>

C:Superfamily: herpesvirus immediate-early protein IE175

C:Keywords: DNA binding; early protein; transcription regulation

Query Match 6.3%; Score 138; DB 1; Length 1460;
Best Local Similarity 22.8%; Pred. No. 0.21; Mismatches 122; Indels 104; Gaps 16;
Matches 76; Conservative 31;

Qy 76 LPTEEEFGLVQSMKCDTVRIKGVQLGP-----TTAPPLMTSEGNVTABDTEEA 124
Db 9 IETEGNFSQLAAAAA-AAEEGSIASGPDGSGSRRRSGCEDLLFGPGLFSDDAAEA 67
Qy 125 IRAFYVAVAAA-----SAAEAHWRLVLLSGQIHEPIGSGGNIINTNGGRSCQNP 177
Db 68 EAAVLAAAGATRP RPSPSAQQQRHARR-----GSGEIVVLDDEDEDEEPG 114
Qy 178 LPSPDQSPSG--NATTSVTRDNYHLLTEEEFGVWSQMKWSHONKSG-GSVPVVRGPTQE 233
Db 115 SPAAG-SPVGLSIRAPSVT-----SSSGFGPGAPGPGRR 149
Qy 234 PCSESQILKESFVPPTTKENNKQEREDENRLLPPPPVAETVPVSPSVTEIETPLQIRP 293
Db 150 PROHSQ--RQRPGPPAAP-----GARPPPPPPPPPPPPA-----PPAPPAPR 192
Qy 294 TATTAGEPLGCTFTISPAFVHSLNKKRQLELLREVEWPGRGHMAATCKLQVEQD 353
Db 193 RPRGDGPPRGG-TRSVSPGRRG-LGPRRHQS-----QQRWPFRRH----- 232
Qy 354 RTMSLAAAVREAPPPTPGASSEPSVPALPGAD 386
Db 233 -----GGGFLQ-QPPPPGRRRRPAAAPPAE 259

RESULT 2

S58380

probable RNA-directed DNA polymerase (EC 2.7.7.49) - Crithidia fasciculata retrotrans
N:Alternate names: probable reverse transcriptase

C:Species: Crithidia fasciculata

C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Sep-1997

C:Accession: S58380; S58381

R.Gabriel, A.
submitted to the EMBL Data Library, December 1994
A:Reference number: S58380
A:Accession: S58380
A:Molecule type: DNA
A:Residues: 1-2517 <GAB>
A:Cross-references: EMBL:U019151; NID:g624680; PID:g624681
R:Teng, S.C.; Wang, S.X.; Gabriel, A.
Nucleic Acids Res. 23, 2929-2936, 1995
A:Title: A new non-LTR retrotransposon provides evidence for multiple distinct site-specific insertion events
A:Reference number: S58381; MUID:93388509; PMID:7659515
A:Accession: S58381
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1825-2116 <TEN>
A:Cross-references: EMBL:U019151
A:Experimental source: retrotransposon CRE2
C:Genetics:
A:Mobile element: retrotransposon CRE2
C:Keywords: nucleotide transferase

Query Match 5.9%; Score 128; DB 2; Length 2517;
Best Local Similarity 21.4%; Pred. No. 2;
Matches 90; Conservative 41; Mismatches 156; Indels 134; Gaps 19;

QY 5 SYVVLCGMKQLGOALQASVLSIITENQKRCPCGAGNLMTCQNPLPSVSHRSPGCGN 64
DB 1123 SIVDAIRMKKEISTTDLTAALGIRKQTSDACPVCDAMQSTIQH-----VPGK 1172
QY 65 AAV-----SVTGGDCHLPTTEEEFVGVOSMKCDIVIRKGVLOGPTTAPPLMTSGNVA 118
DB 1173 AVNFSIEEATATGNQI-----TTTV-----APPTFTHK-----A 1201
QY 119 EDTEEAIRAFVAVAAASAAEAHWHRLVLLSGQTHEPIGSGNIN-----TNKGRSC 173
DB 1202 PNGAEVTRSLLAVIDTTGPEA-----QVHRVTANGTAQAQKCKVLPGEQGE 1250
QY 174 QNPALPSPQPSGN-----ATTSVTRDNYHLLTTEEEFGVWSQMKWHSQNSK 221
DB 1251 TKPTVP-----PKGNLLCYLHKPRVTQTAQRTEDDDHRTTNE-EISSSSHOAPKKRER 1304
QY 222 GGSVPVGRGTQEP--CSESQILKESFVPTTP-----KENNKQEREDENWRLPPPPVAET 274
DB 1305 PASSTTTPSPMPCNSKSEVKI-----DTTPGRQRPHNREEQTRTARAPTYTDNA 1357
QY 275 PVPSVSVTEIETPQRIPTATIAEPLGHCTFTISPAFVHSLNKRKQLELLREVEW 334
DB 1358 ANENASARKREE--QR-----GPIGGATST-SPVINS-----SADFSWVEDTAT 1400
QY 335 PGRGHMAATCCKLQVEGDRTMSLAAAP-----VREAPPPPTGASSEP 377
DB 1401 PIQRTMSFTLDPLSPDEDE-----AVAPDPFLASIVQVVEEDEGTAEAPSMNNGENSEP 1455
QY 378 S 378
DB 1456 A 1456

RESULT 3

A44453
translation initiation factor eIF-4 gamma - human
C:Species: Homo sapiens (man)
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 08-Dec-1994
A:Title: Amino acid sequence of the human protein synthesis initiation factor eIF-4 gamma
A:Reference number: A44453; MUID:93054654; PMID:1423670
A:Accession: A44453
R:Yan, R.; Rychlik, W.; Etchison, D.; Rhoads, R.E.
J. Biol. Chem. 267, 23226-23231, 1992
A:Title: Amino acid sequence of the human protein synthesis initiation factor eIF-4 gamma
A:Reference number: A44453
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-1396 <YAN>
A:Note: sequence inconsistent with the nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBIP:118286)

Query Match 5.6%; Score 121.5; DB 2; Length 1396;
Best Local Similarity 24.1%; Pred. No. 2.6;
Matches 60; Conservative 28; Mismatches 92; Indels 69; Gaps 11;

QY 167 NKGGRSCONPALPSPDQSPSGNATTSVTRDNYHLLTTEEEFGVWSQMKWHSQNSKSGGVP 226
DB 40 SQCAIADRPGLPGPEHSPS-----ESQPSSPSPPT 70
QY 227 VRGPTQEPCESEQILKESFVPT-----TPKENNKQERE-DENWRLPPPPVAETPVSP 279
DB 71 SPSVPLEPGESEPNLAVSLIPGDTMTTIQMSVEESPISRETGEYRLSPSE---TPLAEP 127
QY 280 SVTEIETPLQRIPTATIAEPLGHCTFTISPAFVHSLNKRKQLELLREVEWPGRGH 339
DB 128 -ILEVEVTLSPVPESEFSSPQAPT---PLASHTV-----EIHEP-NGM 168
QY 340 MAATCCKLQVEGDRTMSLAAAPVREAPP--PT-----GASSEPSVPALPGADPQR 389
DB 169 VPSEDEPEVESSPELAPPAC-SESPVPIAPTQAPELLNGAPSPPAVDLSPVSEPEE 227
QY 390 SRELLLLAV 398
DB 228 QAKEVTASV 236

RESULT 4

T49316
profilaggrin related protein [Imported] - Neurospora crassa (fragment)
N:Alternate names: protein B13N20.10
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: T49316
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
submitted to the Protein Sequence Database, May 2000
A:Reference number: Z25022
A:Accession: T49316
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1386 <SCH>
A:Cross-references: EMBL:AL355925; GSPDB:GN00116; NCSP:B13N20.10
A:Experimental source: BAC clone B13N20; strain OR74A
C:Genetics:
A:Gene: NCSP:B13N20.10
A:Map position: 6

Query Match 5.5%; Score 120; DB 2; Length 1386;
Best Local Similarity 18.6%; Pred. No. 3.3;
Matches 94; Conservative 66; Mismatches 144; Indels 202; Gaps 23;

QY 53 LPSVSHRSPPGNAAY-----SVTGG-----DCHLPTTEE----- 81
DB 637 IPEISLQGPENASLRPGPEVLDROSQANGKVSQSGALSERQHLPTQGEAEKLGTTT 696
QY 82 FGVLVQSMKCDT-VRIKGVLOGPTTAPPLMTSEGNVTAEDTEEAIRAFVAVAAASAAEA 140
DB 697 IGRVPSQRLSVPSQKPPQPSPLGTAPVLQSGSSRLQPAQVRLHSSSIIGSSSPQ- 755
QY 141 WHWRLVLLSGQIHEPIGSGN-----IINTNKGGRSCONPALPSPQSPSG 187
DB 756 -----SGSIYTPVQKQNFTEVRRPGAKLPLFERDGGTKGTGTALPLK9HSSG 806
QY 188 NATT--SVTRDNYHLLTTEEEFGVW-----SQSMKWHSQNSKSGSVVVRGPTQEP 234
DB 807 POTTNSITDRPKQLL-----FGKESIKLFSDDPPAKSVVEYGENEENEE---QSPEDM 859
QY 235 CSQSQIL-----KESFVPP---TTPKENNKQEREDENWRLPPPPVAETPV- 278
DB 860 DDYDEIVELEEEQSSAESEFEPPLRLSLDKNSSPIKS-----ALRPPTKGHTPGRAVQFA 915
QY 279 PSVTEIETPQRIPTATIAEPLGHCTFTISPAF-----VHSLNKRK----- 322

Db 476 ASPTHPAPVSTIAPSVTPSRKPIQIPIPLPQAAAPSNPKIPLTTPSPSPATAAAP---T 532
QY 306 TTTTSPAFVHSLVNLKRRKQLELLREVEWPGRGHMAATCKKLQVGEQDRTMSLAAAP--- 362
Db 533 TTTLSPPPTQ-----QQPQS--AAPAPSLLPQQQPTPSAAPAPSL 573
QY 363 VREAPPPPTGASSEPSVP-----ALPGADP 387
Db 574 LQQQQPPPSAARAPSLPPQQQLPFSATP 602
RESULT 8
T18289
racGAP protein - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C:Accession: T18289
R:Judson, S.B.; Eccleston, J.; Strom, M.
J. Biol. Chem. 272, 15682-15685, 1997
A:Title: Cloning of a rhoGAP homolog from Dictyostelium discoideum.
A:Reference number: Z18858; MUID:97332648; PMID:9188459
A:Accession: T18289
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1335 <LUD>
A:Cross-references: EMBL:Y10159; NID:g2190354; PIDN:CAA71241.1; PID:g2190355
C:Genetics:
A:Gene: racGAP
A:Introns: 113/1; 205/3
Query Match 5.3%; Score 115.5; DB 2; Length 1335;
Best Local Similarity 20.3%; Pred. No. 6.4;
Matches 69; Conservative 49; Mismatches 155; Indels 67; Gaps 12;
QY 16 LQALQASVLSLIITENQKRCPCGAQ-NLMTQNPLPVSVSHRSPGCGNAVSVTGGDC 74
Db 179 LQIMEDSAIVTSIIKTVEFISFKQSNHLSTIDIPISVSLPKSPNSVSVS-SGGDS 237
QY 75 -----HLPTEEFGVLQSMKCDTVRIKVLQGP----- 103
Db 238 VSSLBEENLYATALPYQASQGWHLFFKDDKIVLIDIKSEGWLKGELNGKIGFFPASY 297
QY 104 ----TTAPPLMTSEGNVTAE--DTEAIRAFVYAVAAASAPAWHRLVLLSGOIHPEI 157
Db 298 VEIIAIPPVGVPTQLIPDPDSQDLSTISSPILSSSTTS-----SSISIDS 348
QY 158 GSGGNIINTKGRSQCPALSPQSPGSGNATTSVTRDNYHLLTEEEFGVWSQS----- 212
Db 349 NLSSNNNNNNNNNNSTPILSS--TSTTTTTTTNNNNNNNTFPQISVSKSSFSKS 406
QY 213 -MKWHSQKSGSVVRGPTQPCSESQLKESFPPTTPKENNKOEREDENWRLPPPV 271
Db 407 TISTNPSSKSSNLLISNP--PPVKNSTTATSSPDIT-----KLIARPNKLIAPPPL 459
QY 272 AETPVPSVTEIEPTLORIPRTATAGEPLGHCTFTTSP 311
Db 460 VPPTETAPPPLSAPPPL--ISRTSTLTSS--SNTAFTAPP 495
RESULT 9
S76563
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S76563
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76563

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-501 <KAN>
A:Cross-references: EMBL:D64002; GB:AB001339; NID:g1001612; PIDN:BAAL0409.1; PID:g101
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
Query Match 5.2%; Score 114.5; DB 2; Length 501;
Best Local Similarity 23.7%; Pred. No. 2.2;
Matches 94; Conservative 42; Mismatches 121; Indels 139; Gaps 24;
QY 36 RCPFCGAQNLMTQNPTLPSV-----SHRS---PPGNAASVVTGGDCHL---PTEEEFGVL 85
Db 163 RLPITG-----PPIPSLPRFPSTRIQIPRPPGLFAPTPDQGMNPLGPGNRPDFGL 213
QY 86 VQSMKCDTVRIKVLQGPPT-APPLMTSEGNVTAEDE-EAIRAFVYAVAAASAAEAHW 143
Db 214 PPSQ--GTGFTIAPQGITPQEPGLRAEG-----EDTSPEKLENT-LVSTAAQOQALKA 266
QY 144 RHLVLLSGOIHPEIGSGGNIINTKGRSQCN--PALSPQSPGSGNATTSVTRDNYHLL 201
Db 267 KDTI--SG-AVPPI-----ACRNRTEATVVYVNFPSGQK-----DIV 300
QY 202 TEEERGVWSQSMKHSQKSGSVVRGPTQPCPS---ESQIL--KESFVPPPTTKENNK 256
Db 301 GRSYPIIFNQLAQIAIANTYGE-----PTQVTVSFKYDAEICGGVDQFIP- 347
QY 257 OEREDENWRLP--PPVVAETPV---PSPSVTEIETPLQRI-RTATIAIEPLGH 304
Db 348 -GGETTNPVPTVPTPSQVTPAPTISPAGIAPSPAPLQPTPPPAVRSPPMPDAPAPR 406
QY 305 CTTFTISPAFVHSLVNLKRRKQLELLREVEWPGRGHMAATCCKLQVGEQDRTMSLAAAPVR 364
Db 407 RQPTTTPS-----DPPMNVAPSPTR 426
QY 365 EAPPP-----PTGASSEPSVPALPGADPQRSAILL 395
Db 427 SAPAPAPTATPTTSPQSLPKTKG-----EMLL 455
RESULT 10
T38236
hypothetical protein SPAC23A1.17 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T38236
R:Murphy, L.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 1998
A:Reference number: Z21780
A:Accession: T38236
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1611 <MUR>
A:Cross-references: EMBL:AL021813; PIDN:CAA16991.1; GSPDB:GN00066; SPDB:SPAC23A1.17
A:Experimental source: strain 972h.; cosmid c23A1
C:Genetics:
A:Gene: SPDB:SPAC23A1.17
A:Map position: 1
Query Match 5.2%; Score 114; DB 2; Length 1611;
Best Local Similarity 22.4%; Pred. No. 10;
Matches 96; Conservative 35; Mismatches 168; Indels 130; Gaps 19;
QY 17 GOALQASVLSLIITENQKRCPCFCGAQNLMTQNPTLP-----SVSHRSP-PGNAAV 67
Db 804 GSQLRNVVPSIVT--SSGR-----FALPDEMASPSSSICHPLPSPPPADF 847
QY 68 SVTGGDCHLP-----TEEEFGVLVQSMKCDTVRIKVLQGPPTAPPLMTS 112
Db 848 NSLNVDFEPEHSYLSPEAPQPSVEEESFNAT-----VIHAPT--PSTATF 892
QY 113 EGNVT-----AEDTEAIRAFVYAVAAASAAEAHWRLVLLSGOIHPEIGSGNI 163
Db 893 QGHPTISNVTPPLKQDVTESKASPVADASATHQSSTGLTQETQLGSMRLPT-----KL 948

Db 77 KCENMHVQVAPLAPVEEPKATQKQSSANAEAPSVDPSNFTTIHDAVEDCDGGLAPLIG 136
QY 128 FYVAASAAABAW-----HWRLVLLSGIHEPIGSGNIIN---TNKGGRSQNP 176
Db 137 FRYKVCQSNYDLCKKCELAHKHPELML-----RMPTNNGCMVDWFTGGRSRGHC 191
QY 177 ALPSPQSPGNATTSVTRDNYHLLTEEEFGVWSQSMKWHQO---NKSGSVFVR----- 228
Db 192 FQETNQADPAGEPARDSRRERQ--ARRHAGVLSQFVEMMTNPLNLTATTATAPAEPPQPK 249
QY 229 -----GTPQPCSESIQLKESFVPPPTPKENNKQEREDENWRLLPPVAETPPVPSV 281
Db 250 AAEQTESPPQAEPTVTAERAESEAKTEPKKVNTDQ-----SVPRTEDPVTPRS 300
QY 282 TELETPLQRIPTATITAGEPLGCHTFTTISPAFVHS---VLNKRKRGLELLREVEWPGRG 338
Db 301 TQPTPVINDNISQI-----VPEYMRAGIELLNFSEMFSLIITTEGGDSG 349
QY 339 HMAATCC-----KLQVEGQDRMTSLAAAPVREAPPPPTGASSEPSVPALPGADPORS 392
Db 350 IFAPSTPSAENKPKPEQSQSQSGASSANQSAVPSAAPSANQATPSIGSIPDAQLE 409
RESULT 14
S43768
transcription activator Vp1 - rice
C:Species: Oryza sativa (rice)
C:Date: 10-Dec-1994 #sequence_revision 26-May-1995 #text_change 20-Jun-2000
C:Accession: S43768; S48899
R:Hattori, T.; Terada, T.; Hamasuna, S. T.
Plant Mol. Biol. 24, 805-810, 1994
A:Title: Sequence and functional analyses of the rice gene homologous to the maize Vp1.
A:Reference number: S43768; MUID:94250843; PMID:8193305
A:Accession: S43768
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-728 <HAT>
A:Cross-references: EMBL:D16640
A:Experimental source: strain Nipponbare
R:Hattori, T.; Terada, T.; Hamasuna, S.
submitted to the EMBL Data Library, July 1993
A:Description: Sequence and functional analysis of the rice gene homologous to the maize Vp1.
A:Reference number: S48899
A:Accession: S48899
A:Molecule type: DNA
A:Residues: 1-670, 'p', 672-683, 'p', 685-728 <HAW>
A:Cross-references: EMBL:D16640; NID:g391884; PIDN:BAA04066.1; PID:g391885
A:Experimental source: strain Nipponbare
C:Genetics:
A:Gene: Vp1
A:Introns: 526/3; 556/3; 590/2; 606/1; 631/3
C:Superfamily: rice transcription factor Vp1
C:Keywords: DNA binding; transcription factor
Query Match 5.1%; Score 111; DB 2; Length 728;
Best Local Similarity 22.2%; Pred. No. 6.1;
Matches 67; Conservative 29; Mismatches 114; Indels 92; Gaps 15;
QY 170 GRSCONPALSPD-----QSPSGN-----ATTSVTRDNYHLLTEEEFGVWSQSMKWHQO 218
Db 257 GAASDPQPLPSGANPGYEFPSGGGEMGSAATS-----WMPYQAFTPP 300
QY 219 NKSGSVVVRG-----PTQPCSESIQLKES--FVPTTPPKENNKQEREDENWRLLP----- 267
Db 301 AAYGDAMTPGAGFPFQSCSKSVVSSQFPFPTAAAAGDMHASGGNWNWQFPA 360
QY 268 PPVVAETPVPSVTEIETPLQRIPTATITAGE-PLGHCTFT-----ISPAFVHSLYNK- 320
Db 361 PFPVST--SSYTMPSSVVP-----PFTAGFPQYSGGHAMCSPRLAGVPSSTKEARKKR 414
QY 321 --RKROLELLREVEWPGRGHMAATCCCKLQVEGQDRMTSLAA----- 361
Db 415 MARQRRLSLQOO-----RSQOLNLSQIHISGHPOEPSRAAHSAVPVTPSSAGCRSWGI 468

QY 362 -----PVREAPPPTTGASSEPS-VPALPGADPORSAELELLLVATREGLERRIISR 410
Db 469 WPPAAQIIONPLSNPNPPATSKOPKPKPQAAA-----TAGAESLQSTASE 523
QY 411 KR 412
Db 524 KR 525
RESULT 15
C56695
transducin-like enhancer-of-split homolog TLE-2 - human
C:Species: Homo sapiens (man)
C:Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 26-May-2000
C:Accession: C56695
R:Stifani, S.; Blumuelier, C.M.; Redhead, N.J.; Hill, R.E.; Artavanis-Tsakonas, S.
Nature Genet. 2, 119-127, 1992
A:Title: Human homologs of a Drosophila enhancer of split gene product define a novel A:Reference number: A56695; MUID:93265135; PMID:1303260
A:Accession: C56695
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-743 <STI>
A:Cross-references: GB:M99436; NID:g307511; PIDN:AAA61193.1; PID:g307512
C:Genetics:
A:Gene: GDB:TLE2; ESG: ESG2
A:Cross-references: GDB:228048; OMIM:601041
A:Map position: 19p13.3-19p13.3
C:Superfamily: unassigned WD repeat proteins; WD repeat homology
C:Keywords: nucleus
F:499-532/Domain: WD repeat homology <WD1>
F:585-618/Domain: WD repeat homology <WD2>
F:667-700/Domain: WD repeat homology <WD3>
F:708-741/Domain: WD repeat homology <WD4>
Query Match 5.1%; Score 110.5; DB 2; Length 743;
Best Local Similarity 21.1%; Pred. No. 6.7;
Matches 87; Conservative 54; Mismatches 143; Indels 129; Gaps 20;
QY 14 KOLGALQASVLSIITENQGRKCFPCGAQNLMTQNTLPSVSHRSPGNAAVSTGSD 73
Db 101 QOVLOAVERAKQTV-----GELNSLIGQQ--LQPLSHAPP----- 135
QY 74 CHLPTEEEFGLVQSMKCDTVRIKGVLOGPTTAPPLMTSEGNVTAEDTEAI-----RAFV 129
Db 136 --VPL-----TPRAGLVGSGATG--LLALSGALAAQAALAAVKEDRAGV 177
QY 130 YAV-----AAASAAEAHWRLVLLSGIHEPIGSGNIINTNKGGRSQNPALSPDQ 183
Db 178 EAEGSRVERAPRSASPSPPESLV---EERPSGPGG-----GGKQ-----RADEK 220
QY 184 SPSGNATTSVTRDNYHLLTEEEFGVWSQSMKWHQSKSGSVVP-----RGPTQPCSES 238
Db 221 EFSGYSEDEKSDYNLVVDE-----QPSEPPSPATPCGKVPICIPARRDLVDPASIA 276
QY 239 QLKESF-----VPTTPPKENNKQEREDENWRLLPPVPAETPVPSVTEIETPL 288
Db 277 SLRSPLPRAKELIINDLPASTPASKSCDS-----SPQDASTPGPSSASHLCQAL 328
QY 289 QRIPRTATIA-GEPLGHCTFTTISPAFV-----HVLNKRKRGLELLREVEWPGRG--- 338
Db 329 KPAPSTDVSVALRSLP-----TLSSPFTTSLGSHSTLN-----GDLSPSPSVYS 373
QY 339 HMAATCCCKLQVEGQDRMTSLAAAPVREAPPPPTGASSEPSVPALPGADPORS 390
Db 374 LHLSPQSVSSVYGRSPVMAF-----ESHPLRGSSVSSSLPSIPGGKPAYS 420
Search completed: December 25, 2002, 01:14:13
Job time : 50 secs